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SEQUENCE LISTING

<110> ReproCELL Inc., and EMA, Hideo

<120> PROTEIN SUSTAINING UNDIFFERENTIATED STEM CELLS

<130> TR001PCT

<140> PCT/JP02/02285

<141> 2002-3-11

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 1140

<212> DNA

<213> Mus musculus

<400> 1

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<211> 379

<212> PRT

<213> Mus musculus

<400> 2

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Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140
Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
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Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
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 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
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 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
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 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
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 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
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 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
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 Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
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 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
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 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
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 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
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 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
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 <212> DNA
 <213> Rattus norvegicus

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 <212> PRT
 <213> Rattus norvegicus

<400> 6

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35 40 45
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ser Gly Gln
85 90 95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
115 120 125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140
Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
145 150 155 160
Gly Asn Pro Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
180 185 190
Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
195 200 205
Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
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Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
225 230 235 240
Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
245 250 255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
260 265 270
Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
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Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
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Thr Cys His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly
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Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
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<212> DNA
<213> Xenopus sp.

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<211> 374
<212> PRT
<213> Xenopus sp.

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35 40 45
Asp Ile Leu Ile Val Ala Glu Gly Lys Met Ala Pro Phe Thr His Asp
50 55 60
Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile Pro Val Asn Ile His
65 70 75 80
Ala Met Asn Phe Thr Trp Gln Ala Thr Gly Gln Ala Glu Tyr Phe Tyr
85 90 95
Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro
100 105 110
Thr Val Asn Met Pro Leu Leu Gly Thr Val Pro His Lys Ala Thr Val
115 120 125
Ile Gln Val Gly Phe Pro Cys Leu Gly Asn Gln Asp Gly Val Ala Ala
130 135 140
Phe Glu Val Asn Val Ile Val Met Asn Ser Glu Gly Asn Val Ile Leu
145 150 155 160
Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala Lys
165 170 175
Cys Thr Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Asp Arg His Val
180 185 190
Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu

195 200 205
 Cys Met Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Leu
 210 215 220
 Cys Ile Cys Pro Pro Gly Tyr Tyr Gly Ile Asn Cys Asp Lys Val Asn
 225 230 235 240
 Cys Thr Thr His Cys Leu Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys
 245 250 255
 Cys Ile Cys Pro Ser Gly Tyr Glu Gly Glu Gln Cys Glu Thr Ser Lys
 260 265 270
 Cys Gln Gln Pro Cys Arg Asn Gly Gly Lys Cys Ser Gly Lys Asn Lys
 275 280 285
 Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val
 290 295 300
 Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Ile Glu Pro Asn Lys
 305 310 315 320
 Cys Gln Cys Lys Glu Gly Trp Asn Gly Arg Tyr Cys Asn Lys Lys Tyr
 325 330 335
 Gly Ser Asn Leu Met Asn Ala Leu Arg Pro Thr Gly Ser Arg Asn Arg
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 Glu Ser Asn Tyr Ile Trp
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 <212> DNA
 <213> Danio rerio

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<210> 10
 <211> 378
 <212> PRT.
 <213> Danio rerio

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 35 40 45
 Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala Pro Phe
 50 55 60

Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile Pro Val
 65 70 75 80
 Asn Ile His His Val Asn Phe Thr Trp Gln Ala Thr Asp Gln Ala Glu
 85 90 95
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 115 120 125
 Ala Ser Val Val Gln Val Gly Phe Pro Cys Arg Gly Asp Gln Asp Gly
 130 135 140
 Val Ala Ala Phe Glu Val Thr Ile Leu Val Met Asp Ala Gly Gly Asn
 145 150 155 160
 Ile Ile Leu Arg Thr Pro His Asn Ala Ile Phe Phe Lys Thr Cys Gln
 165 170 175
 Arg Ala Lys Cys Pro Gly Gly Cys Arg Asn Gly Gly Tyr Cys Asn Glu
 180 185 190
 Arg Gln Val Cys Glu Cys Gln Asp Gly Phe Tyr Gly Val His Cys Glu
 195 200 205
 Lys Ala Leu Cys Ser Pro Arg Cys Leu Asn Gly Gly Leu Cys Met Ser
 210 215 220
 Pro Gly Val Cys Ile Cys Pro Pro Gly Tyr Phe Gly Ser Ser Cys Glu
 225 230 235 240
 Arg Ala Asn Cys Ser Thr Thr Cys Leu Asn Gly Gly Thr Cys Phe His
 245 250 255
 Pro Gly Lys Cys Ile Cys Ala Val Ser Phe Glu Gly Val Arg Cys Glu
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 Leu Ser Lys Cys Arg Gln Pro Cys Arg Asn Gly Gly Lys Cys Thr Gly
 275 280 285
 Arg Asn Lys Cys Lys Cys Ser Lys Gly Tyr His Gly Asp Leu Cys Ser
 290 295 300
 Lys Ala Val Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Val Glu
 305 310 315 320
 Pro Asn Arg Cys Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn
 325 330 335
 Lys Arg Phe Arg Gly Gly Val Ser Asn Ser Gln Arg Val Ser Pro Ser
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 <213> Artificial Sequence

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 Sequence

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<210> 12
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<223> Description of Artificial Sequence:Artificial Sequence

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28

<210> 13

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:pCAGGS 6xHis construct.

<400> 13

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gggcaataa tttaaacat cagaatggt atttggttt gatttggga acatagga 2040
tatgttggg gcatgaaa aaggtggtt taagaggtc atcagtat gaaacagccc 2100
cgtctgtcc attcctatt catagaaaa gcttgactt ggggttagt ttttttata 2160
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aattgttat ccgttcaca ttccacaa catagagcc ggaagcata agtgtaagc 2400
ctgggtggt taatgagtg cttaactac attaatgg ttgcgtcac tggccgctt 2460
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ccgcccctaa ctccgccc cccgcccct actcggccc gttccgccc tctccgccc 2580
caggtctgac taattttt tttttatga gggggggg cggctcggc ctctgagca 2640
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gggaagcgt gctgttctc atgtcagc ctgtaggtt ctgattcgg ttaggtcgt 3300
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gtggcctaac tacggctac ctagaaggac agtatttgt atctgcgtc tctgaagcc 3540
agtaccctc ggaanaagag ttgttagct ttgatccgc aaaaaccca ccgctgtag 3600
cgttggttt tttgtttga agcagcagt tacggcaga aaaaagggat ctcaagaga 3660
tctttgata tttctacgg ggtctgagc tcagtgaac gaaactcac gtttagggt 3720
ttgttcatg agattatcaa aaaggtctt cacttagat cttttaaatt aaaaatgaag 3780
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ttttaaatca atctaaagta tataatgagta aacttggctc gacagttacc aalgcttaat 3840
cagtgaggca cctatctcag gcatctgtct atttcgttca tccatagttg cctgacitccc 3900
cgtcgtgtag ataactacga tacggagggg cttaaccatct gcccacagtg ctgcaatgat 3960
accgagagac ccacgcctac cggctccaga ttatcagca ataaaccagc cagccggaag 4020
ggcggagcgc agaagtgtgc ctgcaacttt aiccgctccc atccagttca ttaattgttg 4080
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cactcgtgca cccaactgat cticagcalt tttactttc accagcgttt ctgggtgagc 4620
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actcatactc ttctttttc aatattatg aagcatttat caggtttatt gtctcagag 4740
cggatacata ttgaaatga tttaaaaaa taacanaata ggggttccgc gcacatttcc 4800
ccgaaaagtg ccacctg 4817

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<210> 14
 <211> 1140
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

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<400> 14
atggctcaga gaagagcctt cccgctttc ggcctccggc tctggagcat cctacettgc 60
ctgctccigc tgcagagcga tgcagggcag ccacctgagg azagcttgta cctgaggatc 120
gacgcccac cagctagagt gctcatagga ttgaagaag acctctgat tctctggag 180
gggaaaaatg cccctttac acatgatttc aggaagagcc aacaaagaa gcccgcatt 240
cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggg agaatattc 300
tacgaatttc tctctctgcy cctccctgaa aaagcctca tggcagatcc aactgtcaat 360
gtccctttgc tgggaacagt gccacaaag gcatcagttg ttcaagttg ttcccggtg 420
ctcggcaaac agacagaggt agcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
ggcaacacca tcttaagac cctcagaat gccatcttct ttaaaacalg tcaacagct 540
agtgctccgc gagggtatgc aaatggaggg ttttgtaacg aaagccgggt ctgcagatg 600
ccggaatgggt tctacgggac tcactgtgag aaagcctgt gcatccccc atgtatgaa 660
gttggtctgt gtgtacatc tggcttcgic atctgcccc ctggaattcta cgtgtcaac 720
tgtacaaag caaatctgc aaccaccctc tttaatzgag gacctgctt ttacccgga 780
aaatgtattt gccctctcgg actcgaggga gacagttgt aactcagcaa atgccccaa 840
ccttgccgaa atggaggtta atgcatttgt aaagcagat gtaagtgcgc gaaaggttac 900
caaggagacc tctgtctaa gccctctcgc gacctggtct gtgtgctca cgaacctgc 960
cacgaacca acaagtcca gtgtcagag gctgtgacg gcagacactg caataagag 1020
talgagcca cctcatgca tggccgagg ccagcaggg ccgggtgga gcgacacg 1080
ccttcacta aaagagctga ggaagaagg gatccacctg aatccaatta catctgtga 1140

```

<210> 15
 <211> 379
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

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<400> 15
Met Ala Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15
Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
20 25 30
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45
Ile Gly Phe Glu Glu Asp Leu Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly

```

100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 116 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350
 Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 16
 <211> 1140
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial
 Sequence

<400> 16
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 ctgctcctgc tgcgagcgga tgcagggcng ccacctgagg agagcttcta cctgtggatc 120
 gacggccatc aggcagaggt gcicntagga ttgaagaag acattctgat tctctcggag 180
 aggaanaatg ccccttttac acatgatttc aggaagccc ancanagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcagac agaatacttc 300
 taagagttcc tgtctctcgc ctccatlgat aaaggcatca tgcagatcc aactgtcaat 360
 gtccctttgc tgggaacagt gccctacang gcatcagttg ttcaagttgg ttcccggtgt 420
 ctgcgcaaac agacggggt agcagcattt gaagtgaatg tgattgtcal gaattctgaa 480
 ggcacaccca tccctaggac cccctcagat gccatcttct ttaaaacatg tcaacaagct 540
 gagtgtcccg gagggtatcg aaatggaggt ttttgtaacg aaaggcgggt ctgcagaggt 600
 ccggtatggg tctacgggcc tcacigtagg aaagccctgt gcataccccc atgtatgaac 660
 gttgtctctg gtgtcacctc tggcttctgc atcggccccc ctggtttcta cgggtgtcaac 720
 tggacaaag caaacgtctc aaccacctgc tttaatggag gacactgctt ttaccgggaa 780
 aaatgtattt gccctcctgc actcagggga gacagtggtt aactcagcaa atgccccaa 840
 cctgctcga atggaggtaa atgcattggt aaagcgaatg ttaagtgccc gaaggtttac 900
 caaggagacc tgtgtctcta gccgtctgc gacctggtt gtgtgctcca cggacctgc 960

cacgaaccca acaagtgcga gtgtcgagag gcttcgcagg gcagacactg caataagagg 1020
 taaggagcca gcttcattga tgcctcgagg ccagcaggcg ccggcctgga gcagacacag 1080
 ccttcacitg aaagagctga gcatagagg gatccacctg aatccaatga catctggtga 1140

<210> 17

<211> 879

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 17

Met Ala Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15
 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Ile Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
355 380 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
370 375

<210> 18
<211> 1140
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial
Sequence

<400> 18
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ctgtctctgc tgcagcgga tgcagggcag ccacctgagg agagcttga cctgtggatc 120
gaagcccatc agctagagt gctatagga ttgaagag acattctgat tctctggag 180
gggaaatgg cccctttac acatgattc aggaagccc aacaaagaa gccagccatt 240
cctgtcaata tccctccat gaattttacc tggcaagctg cggggcaggc agaatacttc 300
taccagttcc tctcttggc ctccctggat aaagccatca tggcagatcc aactgtcaat 360
gtccctttgc tggzaacagt gctcacaag gcatcagttg tccaagttag ttccctgtg 420
ctcggcaaac aagacgggtt agcagcattt gaagtaag tgattgtcat gaattctgaa 480
ggcaacacca tctttaggac cctcagaat gccatctctt ttaaacatg tcaacangct 540
gagtgctggc gagggtgtgc aaatggagc ttgtatagc aaagcggtt ctgagagtgt 600
ccgattgggt tctacgggc tcaatgtag aaagccctgt gcataccccc atgtatgaa 660
ggtggtctgt gttctcttc tggcttctgc atctgcccc ctgatttcta cgtgtcaac 720
tgtacaaag taactgtctt aaccacctgc tttaattgag gacactgctt ttacccggga 780
aaatgtattt gcccctctg actgagggg gagcagtggt aactcagaa atgccccaa 840
cccctggga atggagctaa atgcatttgt aaagcnaat gtaagtggc gaaggttac 900
caggagacc tctctctaa gccctgtctc gacctggtt atgtgccc cggaaacctgc 960
cagaaacca acaagtcca gtctgagag gctggcacc gcagacatg caataagagg 1020
taigagcca gccatgca tggccgagg ccagcagcg cgggctgga gcgacacag 1080
cttctactta aaaggtcta ggaagaagg gatccacctg aatccaatia catctggtga 1140

<210> 19
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial
Sequence

<400> 19
Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15
Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
20 25 30
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Arg Met Pro Ala Ile
65 70 75 80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140
Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
145 150 155 160
Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr

165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Val Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350
 Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 20

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Sequence

<400> 20

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 ctgctccctgc tgcgagcga tgcagggcag ccacctgagg agagcttcta cctgtggatc 120
 gacgcccac aggcctagagt gctcatagga ttgaagaag acattctgat tctctcggag 180
 gggaaaatgg ccccttttat acatgatttc aggaagccc aacaaagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggc agaatcttc 300
 tacgaattcc tctctctcgc ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
 gtccctttgc tgggaacagt gcttcacag gcatacattg ttcaagttag ttccctgtgt 420
 ctggcacaac agagcgggt agcagcattt gaagigaatg tgaattgcat gaattctgaa 480
 ggcacaccca tccctaggac ccttcagaaat gccctctctt tttaaaatg tcaacaagct 540
 gagtgtccc gaggtgtgc aaatggaggc ttltgtacgc aaagcgggt ctgagaggt 600
 cggatgggt tctacgggcc tcaatgtgag aagccctgt gataccccc atgtatgaac 660
 ggtatctgt gtgtcactcc tggctctgc atctgcccc ctgattctca cgtgtcaac 720
 tgtgacaang caaatgtgc aaccacctgc tttaatzgag ggacctgctt ttacccggga 780
 aaatgtattt gccctcctgc actcgaggga gatcagtggt aactcagcaa atgccccaa 840
 cctgcggaa atggaggtga atgcattgt aaaaagcaagt gtaagtgcc gaaaggttac 900
 caaggagacc tgtgtcttaa gcccgtctgc gggcttgact atgtgccc cgaacacctc 960
 cagcaacca acaagtcca gtgtcagag gactggcagc ctgagacact caataagagg 1020
 tatggagcca gctcatgca tccccgagg ccagcagctc cgggcttga gcacacacg 1080
 ccttcactta aaaaagctga ggaatgaagg gatccacctg aatccaatta catctggtga 1140

<210> 21

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial

Sequence

<400> 21

Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15
 Ile Leu Pro Cys Leu Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Asp Gln
 260 265 270
 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350
 Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365
 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 22

<211> 558

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 22

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atgctcggga gaagagcctt ccttgccttc gcctccggc tcggagcat cctaccttgc 60
ctgctccigc tgcagcgga tgcagcgga ccaccigagg agagcttga cctgtggatc 120
gaccccaic agcttagat gctcatagga ttgaagag acattctgat tctctggag 180
gggaaatgg cccctttac acaatgllc aggaagccc acaagagat gccagccatt 240
cctgtcaata tccactccat gaattttacc tggcaagctc cgggacagac agaatacttc 300
tacgagttcc tctctctgca ctccctggat aaagcctca tggcagatcc aactgtcaat 360
gtccctttgc tgggaacagt gccacacag gcacagttg ttcaagttgg ttccctgtgt 420
ctcggcaaac aagacggggt agcagcattt gaagtgatg tgattgtcat gaattctgaa 480
ggaaacacca tccitaggac ccttcagaat gccatcttct ttaaaacaca gctagcccat 540
catcatcctc atcattga
558

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<210> 23

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 23

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Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15
Ile Leu Pro Cys Leu Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
20 25 30
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140
Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
145 150 155 160
Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
165 170 175
Gln Leu Ala His His His His His
180 185

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<210> 24

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 24

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 Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg Arg Val Cys
 35 40 45
 Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu Cys
 50 55 60
 Ile Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Phe Cys
 65 70 75 80
 Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn Cys Asp Lys Ala Asn Cys
 85 90 95
 Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys Cys
 100 105 110
 Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln Cys Glu Leu Ser Lys Cys
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 Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys Ile Gly Lys Ser Lys Cys
 130 135 140
 Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val Cys
 145 150 155 160
 Glu Pro Gly Cys Gly Ala His Gly Thr Cys His Glu Pro Asn Lys Cys
 165 170 175
 Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Gly
 180 185 190
 Ala Ser Leu Met His Ala Pro Arg Pro Ala Gly Ala Gly Leu Glu Arg
 195 200 205
 His Thr Pro Ser Leu Lys Lys Ala Glu Asp Arg Arg Asp Pro Pro Glu
 210 215 220
 Ser Asn Tyr Ile Trp Gln Leu Ala His His His His His His
 225 230 235